OM of: US-09-972-467-2_COPY_289_478 to: GenEmbl:* out_format : pfs

Date: Jun 20, 2002 6:50 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09972467/runat_20062002_105946_2165/app_query.fasta_1.2455
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=50 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=25 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09972467_@CGN1_1_19316
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-972-467-2_COPY_289_478
Query length: 190
Database: GenEmbl:*
Database sequences: 1797656
Database length: 1873333701
Search time (sec): 7733.930000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation
gb_pr:AB037733	+	1031.00	2072.63	4.4e-107	5139	! AB037733 Homo sapiens mRNA for
gb_pat:AX319857	+	1031.00	2071.45	5.1e-107	5808	! AX319857 Sequence 21 from Pate
gb_pr:AF261918	+	1025.00	2063.58	1.4e-106	3674	! AF261918 Homo sapiens disinteg
gb_pat:AX319858	+	655.00	1305.10	2.5e-64	4518	! AX319858 Sequence 22 from Pate
gb_in:CET13H10	-	590.00	1153.83	6.6e-56	30601	! Z69361 Caenorhabditis elegans
gb_ro:D67076	+	562.50	1116.73	7.7e-54	4180	! D67076 Mouse mRNA for secretor
gb_ro:AF149118	+	562.50	1115.24	9.3e-54	4878	! AF149118 Rattus norvegicus a c
gb_pat:E29966	+	559.50	1116.83	7.6e-54	2184	! E29966 Human ADAMTS-1 protein,
gb_ro:AF304446	+	555.50	1106.07	3.0e-53	2857	! AF304446 Rattus norvegicus ADA
gb_pat:E58656	+	550.50	1095.86	1.1e-52	2853	! E58656 Novel metallic protease
gb_pr:AF060152	+	550.50	1094.09	1.4e-52	3430	! AF060152 Homo sapiens METH1 pr
gb_pat:E29406	+	550.50	1092.58	1.7e-52	4014	! E29406 Novel integrin ligand I
gb_pr:AB037767	+	550.50	1091.90	1.9e-52	4309	! AB037767 Homo sapiens mRNA for
gb_pr:AF170084	+	550.50	1091.60	1.9e-52	4447	! AF170084 Homo sapiens metallop
gb_pr:AF207664	+	550.50	1091.15	2.1e-52	4659	! AF207664 Homo sapiens matrix m
gb_pat:AX342635	+	519.50	1032.22	3.9e-49	2930	! AX342635 Sequence 32 from Pate
gb_pat:AX319860	+	519.50	1032.20	3.9e-49	2937	! AX319860 Sequence 24 from Pate
gb_pr:AF175283	+	513.00	1032.16	4.0e-49	739	! AF175283 Homo sapiens zinc meta
gb_pr:AF060153	+	513.00	1016.66	2.9e-48	3711	! AF060153 Homo sapiens METH2 pr
gb_pat:E55282	+	509.00	1011.65	5.5e-48	2670	! E55282 Novel metalloprotease a
gb_pat:E58655	+	509.00	1011.65	5.5e-48	2670	! E58655 Novel metallic protease
gb_ro:AF175282	+	503.00	996.41	3.9e-47	3638	! AF175282 Mus musculus zinc met
gb_pr:HSA250725	+	490.00	966.55	1.8e-45	5115	! AJ250725 Homo sapiens mRNA for
gb_pr:AF140675	+	489.00	969.08	1.3e-45	3179	! AF140675 Homo sapiens zinc met
gb_pat:E55265	+	489.00	964.61	2.3e-45	5061	! E55265 Novel metalloprotease a
gb_pat:AX128433	+	489.00	964.07	2.5e-45	5353	! AX128433 Sequence 2 from Paten
gb_ro:AB042271	+	483.00	965.77	2.0e-45	1251	! AB042271 Rattus norvegicus mRN
gb_pr:AF148213	+	482.00	952.11	1.1e-44	4193	! AF148213 Homo sapiens aggrecan
gb_pr:AB014588	+	482.00	951.86	1.2e-44	4301	! AB014588 Homo sapiens mRNA for
gb_ro:AF140673	+	460.50	911.36	2.1e-42	3002	! AF140673 Mus musculus putative
gb_pr:AF140674	+	459.50	909.82	2.6e-42	2848	! AF140674 Homo sapiens zinc met
gb_pr:AF142099	+	454.50	893.22	2.2e-41	5533	! AF142099 Homo sapiens aggrecan
gb_pat:AX327757	+	453.00	898.00	1.2e-41	2445	! AX327757 Sequence 13 from Pate
gb_pat:AX327754	+	453.00	895.62	1.6e-41	3132	! AX327754 Sequence 10 from Pate
gb_pat:E55273	+	453.00	895.08	1.7e-41	3312	! E55273 Novel metalloprotease a
gb_pat:AX327752	+	453.00	895.03	1.7e-41	3329	! AX327752 Sequence 8 from Paten
gb_pat:AX327755	+	453.00	894.63	1.8e-41	3471	! AX327755 Sequence 11 from Pate
gb_pat:AX319851	+	452.00	893.04	2.2e-41	3312	! AX319851 Sequence 15 from Pate
gb_pr:AF163762	+	445.00	878.47	1.4e-40	3400	! AF163762 Homo sapiens zinc met
gb_pat:AX319852	+	439.50	866.48	6.7e-40	3675	! AX319852 Sequence 16 from Pate
gb_pat:AX327747	+	438.50	865.74	7.4e-40	3207	! AX327747 Sequence 3 from Pa
gb_pat:AX338539	+	438.50	865.18	7.9e-40	3402	! AX338539 Sequence 3 from Pa
gb_pat:AX327745	+	438.50	865.17	7.9e-40	3403	! AX327745 Sequence 1 from Pa
gb_pat:AX338537	+	438.50	865.17	7.9e-40	3403	! AX338537 Sequence 1 from Pa
gb_pat:AX319854	+	395.50	779.11	4.9e-35	2805	! AX319854 Sequence 18 from P
gb_ro:AB001735	+	393.50	763.56	3.6e-34	9248	! AB001735 Mus musculus DNA f
gb_pr:AP001599	-	386.00	723.75	6.0e-32	118241	! AP001599 Homo sapiens gen
gb_pr:AP001598	-	386.00	720.20	9.4e-32	171038	! AP001598 Homo sapiens gen
gb_pr:AP001697	-	386.00	713.60	2.2e-31	340000	! AP001697 Homo sapiens gen
gb_htg:AC095131	+	382.50	713.40	2.3e-31	164800	! AC095131 Rattus norvegicu

seq_name: gb_pr:AB037733

seq_documentation_block:

```
LOCUS       AB037733               5139 bp    mRNA    linear   PRI 14-MAR-2000
DEFINITION  Homo sapiens mRNA for KIAA1312 protein, partial cds.
ACCESSION   AB037733
VERSION     AB037733.1  GI:7242978
KEYWORDS    .
SOURCE      Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
            clone:fh11767.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Nagase,T., Kikuno,R., Ishikawa,K.I., Hirosawa,M. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XVI. The complete sequences of 150 new cDNA clones from brain which
            code for large proteins in vitro
  JOURNAL   DNA Res. 7 (1), 65-73 (2000)
  MEDLINE   20181126
REFERENCE   2  (bases 1 to 5139)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
            Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
            Fax:+81-438-52-3914)
FEATURES             Location/Qualifiers
     source          1. .5139
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="fh11767"
                     /tissue_type="brain"
                     /clone_lib="pBluescriptII SK plus"
     gene            1. .4417
                     /gene="KIAA1312"
     CDS             <1. .4417
                     /gene="KIAA1312"
                     /note="Start codon is not identified."
                     /codon_start=2
                     /product="KIAA1312 protein"
                     /protein_id="BAA92550.1"
                     /db_xref="GI:7242979"
                     /translation="NSEHTAVISLCSGMLGTFRSHDGDYFIEPLQSMDEQEDEEEQNK
                     PHIIYRRSAPQREPSTGRHACDTSEHKNRHSKDKKKTRARKWGERINLAGDVAALNSG
                     LATEAFSAYGNKTDNTREKRTHRRTKRFLSYPRFVEVLVVADNRMVSYHGENLQHYIL
                     TLMSIVASIYKDPSIGNLINIVIVNLIVIHNEQDGPSISFNAQTTLKNFCQWQHSKNS
                     PGGIHHDTAVLLTRQDICRAHDKCDTLGLAELGTICDPYRSCSISEDSGLSTAFTIAH
                     ELGHVFNMPHDDNNKCKEEGVKSPQHVMAPTLNFYTNPWMWSKCSRKYITEFLDTGYG
                     ECLLNEPESRPYPLPVQLPGILYNVNKQCELIFGPGSQVCPYMMQCRRLWCNNVNGVH
                     KGCRTQHTPWADGTECEPGKHCKYGFCVPKEMDVPVTDGSWGSWSPFGTCSRTCGGGI
                     KTAIRECNRPEPKNGGKYCVGRRMKFKSCNTEPCLKQKRDFRDEQCAHFDGKHFNING
                     LLPNVRWVPKYSGILMKDRCKLFCRVAGNTAYYQLRDRVIDGTPCGQDTNDICVQGLC
                     RQAGCDHVLNSKARRDKCGVCGGDNSSCKTVAGTFNTVHYGYNTVVRIPAGATNIDVR
                     QHSFSGETDDDNYLALSSSKGEFLLNGNFVVTMAKREIRIGNAVVEYSGSETAVERIN
                     STDRIEQELLLQVLSVGKLYNPDVRYSFNIPIEDKPQQFYWNSHGPWQACSKPCQGER
                     KRKLVCTRESDQLTVSDQRCDRLPQPGHITEPCGTDCDLRWHVASRSECSAQCGLGYR
                     TLDIYCAKYSRLDGKTEKVDDGFCSSHPKPSNREKCSGECNTGGWRYSAWTECSKSCD
                     GGTQRRRAICVNTRNDVLDDSKCTHQEKVTIQRCSEFPCPQWKSGDWSECLVTCGKGH
                     KHRQVWCQFGEDRLNDRMCDPETKPTSMQTCQQPECASWQAGPWGQCSVTCGQGYQLR
                     AVKCIIGTYMSVVDDNDCNAATRPTDTQDCELPSCHPPPAAPETRRSTYSAPRTQWRF
```

```
                    GSWTPCSATCGKGTRMRYVSCRDENGSVADESACATLPRPVAKEECSVTPCGQWKALD
                    WSSCSVTCGQGRATRQVMCVNYSDHVIDRSECDQDYIPETDQDCSMSPCPQRTPDSGL
                    AQHPFQNEDYRPRSASPSRTHVLGGNQWRTGPWGACSSTCAGGSQRRVVVCQDENGYT
                    ANDCVERIKPDEQRACESGPCPQWAYGNWGECTKLCGGGIRTRLVVCQRSNGERFPDL
                    SCEILDKPPDREQCNTHACPHDAAWSTGPWSSCSVSCGRGHKQRNVYCMAKDGSHLES
                    DYCKHLAKPHGHRKCRGGRCPKWKAGAWSQCSVSCGRGVQQRHVGCQIGTHKIARETE
                    CNPYTRPESERDCQGPRCPLYTWRAEEWQECTKTCGEGSRYRKVVCVDDNKNEVHGAR
                    CDVSKRPVDRESCSLQPCEYVWITGEWSEVPSWEL"
BASE COUNT      1471 a    1112 c    1362 g    1194 t
ORIGIN


alignment_scores:
            Quality: 1031.00              Length:    190
              Ratio:  5.426                Gaps:      0
 Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
 US-09-972-467-2_COPY_289_478 x AB037733   ..

 Align seg 1/1  to: AB037733  from: 1  to: 5139

      1 LeuSerTyrProArgPheValGluValLeuValValAlaAspAsnArgMe 17
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    392 TTATCCTATCCACGGTTTGTAGAAGTCTTGGTGGTGGCAGACAACAGAAT 441

     17 tValSerTyrHisGlyGluAsnLeuGlnHisTyrIleLeuThrLeuMetS 34
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    442 GGTTTCATACCATGGAGAAAACCTTCAACACTATATTTTAACTTTAATGT 491

     34 erIleValAlaSerIleTyrLysAspProSerIleGlyAsnLeuIleAsn 50
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    492 CAATTGTAGCCTCTATCTATAAAGACCCAAGTATTGGAAATTTAATTAAT 541

     51 IleValIleValAsnLeuIleValIleHisAsnGluGlnAspGlyProSe 67
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    542 ATTGTTATTGTGAACTTAATTGTGATTCATAATGAACAGGATGGGCCTTC 591

     67 rIleSerPheAsnAlaGlnThrThrLeuLysAsnPheCysGlnTrpGlnH 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    592 CATATCTTTTAATGCTCAGACAACATTAAAAAACTTTTGCCAGTGGCAGC 641

     84 isSerLysAsnSerProGlyGlyIleHisHisAspThrAlaValLeuLeu 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    642 ATTCGAAGAACAGTCCAGGTGGAATCCATCATGATACTGCTGTTCTCTTA 691

    101 ThrArgGlnAspIleCysArgAlaHisAspLysCysAspThrLeuGlyLe 117
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    692 ACAAGACAGGATATCTGCAGAGCTCACGACAAATGTGATACCTTAGGCCT 741

    117 uAlaGluLeuGlyThrIleCysAspProTyrArgSerCysSerIleSerG 134
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    742 GGCTGAACTGGGAACCATTTGTGATCCCTATAGAAGCTGTTCTATTAGTG 791

    134 luAspSerGlyLeuSerThrAlaPheThrIleAlaHisGluLeuGlyHis 150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    792 AAGATAGTGGATTGAGTACAGCTTTTACGATCGCCCATGAGCTGGGCCAT 841

    151 ValPheAsnMetProHisAspAspAsnAsnLysCysLysGluGluGlyVa 167
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    842 GTGTTTAACATGCCTCATGATGACAACAACAAATGTAAAGAAGAAGGAGT 891

    167 lLysSerProGlnHisValMetAlaProThrLeuAsnPheTyrThrAsnP 184
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    892 TAAGAGTCCCCAGCATGTCATGGCTCCAACACTGAACTTCTACACCAACC 941

    184 roTrpMetTrpSerLysCys 190
        ||||||||||||||||||||
    942 CCTGGATGTGGTCAAAGTGT 961

        AX319857
```

```
LOCUS       AX319857                5808 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 21 from Patent WO0183782.
ACCESSION   AX319857
VERSION     AX319857.1  GI:17901447
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Plowman,G.D., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S. and
            Payne,V.
  TITLE     Novel proteases
  JOURNAL   Patent: WO 0183782-A 21 08-NOV-2001;
            Sugen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .5808
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      1609 a    1354 c    1540 g    1305 t
ORIGIN


alignment_scores:
            Quality: 1031.00              Length:    190
              Ratio:  5.426                Gaps:      0
 Percent Similarity: 100.000    Percent Identity: 100.000

alignment_block:
 US-09-972-467-2_COPY_289_478 x AX319857   ..

 Align seg 1/1  to: AX319857  from: 1  to: 5808

      1 LeuSerTyrProArgPheValGluValLeuValValAlaAspAsnArgMe 17
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    865 TTATCCTATCCACGGTTTGTAGAAGTCTTGGTGGTGGCAGACAACAGAAT 914

     17 tValSerTyrHisGlyGluAsnLeuGlnHisTyrIleLeuThrLeuMetS 34
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    915 GGTTTCATACCATGGAGAAAACCTTCAACACTATATTTTAACTTTAATGT 964

     34 erIleValAlaSerIleTyrLysAspProSerIleGlyAsnLeuIleAsn 50
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    965 CAATTGTAGCCTCTATCTATAAAGACCCAAGTATTGGAAATTTAATTAAT 1014

     51 IleValIleValAsnLeuIleValIleHisAsnGluGlnAspGlyProSe 67
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1015 ATTGTTATTGTGAACTTAATTGTGATTCATAATGAACAGGATGGGCCTTC 1064

     67 rIleSerPheAsnAlaGlnThrThrLeuLysAsnPheCysGlnTrpGlnH 84
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1065 CATATCTTTTAATGCTCAGACAACATTAAAAAACTTTTGCCAGTGGCAGC 1114

     84 isSerLysAsnSerProGlyGlyIleHisHisAspThrAlaValLeuLeu 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1115 ATTCGAAGAACAGTCCAGGTGGAATCCATCATGATACTGCTGTTCTCTTA 1164

    101 ThrArgGlnAspIleCysArgAlaHisAspLysCysAspThrLeuGlyLe 117
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1165 ACAAGACAGGATATCTGCAGAGCTCACGACAAATGTGATACCTTAGGCCT 1214

    117 uAlaGluLeuGlyThrIleCysAspProTyrArgSerCysSerIleSerG 134
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1215 GGCTGAACTGGGAACCATTTGTGATCCCTATAGAAGCTGTTCTATTAGTG 1264

    134 luAspSerGlyLeuSerThrAlaPheThrIleAlaHisGluLeuGlyHis 150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1265 AAGATAGTGGATTGAGTACAGCTTTTACGATCGCCCATGAGCTGGGCCAT 1314

    151 ValPheAsnMetProHisAspAspAsnAsnLysCysLysGluGluGlyVa 167
        ||||||||||||||||||||||||||||||||||||||||||||||||||
   1315 GTGTTTAACATGCCTCATGATGACAACAACAAATGTAAAGAAGAAGGAGT 1364
```

```
alignment_scores:
            Quality:  422.00              Length:     70
              Ratio:  6.029                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-972-467-2_COPY_509_578 x AF261918   ..

 Align seg 1/1  to: AF261918  from: 1  to: 3674

       1 GlnLeuProGlyIleLeuTyrAsnValAsnLysGlnCysGluLeuIlePh 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1537 CAACTGCCAGGCATCCTTTACAACGTGAATAAACAATGTGAATTGATTTT 1586

      17 eGlyProGlySerGlnValCysProTyrMetMetGlnCysArgArgLeuT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1587 TGGACCAGGTTCTCAGGTGTGCCCATATATGATGCAGTGCAGACGGCTCT 1636

      34 rpCysAsnAsnValAsnGlyValHisLysGlyCysArgThrGlnHisThr 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1637 GGTGCAATAACGTCAATGGAGTACACAAAGGCTGCCGGACTCAGCACACA 1686

      51 ProTrpAlaAspGlyThrGluCysGluProGlyLysHisCysLysTyrGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1687 CCCTGGGCCGATGGGACGGAGTGCGAGCCTGGAAAGCACTGCAAGTATGG 1736

      67 yPheCysVal 70
         |||||||||
    1737 ATTTTGTGTT 1746

seq_name: gb_pr:AB037733

seq_documentation_block:
LOCUS       AB037733               5139 bp    mRNA    linear   PRI 14-MAR-2000
DEFINITION  Homo sapiens mRNA for KIAA1312 protein, partial cds.
ACCESSION   AB037733
VERSION     AB037733.1  GI:7242978
KEYWORDS    .
SOURCE      Homo sapiens brain cDNA to mRNA, clone_lib:pBluescriptII SK plus
            clone:fh11767.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Nagase,T., Kikuno,R., Ishikawa,K.I., Hirosawa,M. and Ohara,O.
  TITLE     Prediction of the coding sequences of unidentified human genes.
            XVI. The complete sequences of 150 new cDNA clones from brain which
            code for large proteins in vitro
  JOURNAL   DNA Res. 7 (1), 65-73 (2000)
  MEDLINE   20181126
REFERENCE   2  (bases 1 to 5139)
  AUTHORS   Ohara,O., Nagase,T. and Kikuno,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
            Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
            292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
            URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
            Fax:+81-438-52-3914)
FEATURES             Location/Qualifiers
     source          1. .5139
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="fh11767"
                     /tissue_type="brain"
                     /clone_lib="pBluescriptII SK plus"
     gene            1. .4417
                     /gene="KIAA1312"
     CDS             <1. .4417
                     /gene="KIAA1312"
                     /note="Start codon is not identified."
                     /codon_start=2
                     /product="KIAA1312 protein"
                     /protein_id="BAA92550.1"
                     /db_xref="GI:7242979"
                     /translation="NSEHTAVISLCSGMLGTFRSHDGDYFIEPLQSMDEQEDEEEQNK
                     PHIIYRRSAPQREPSTGRHACDTSEHKNRHSKDKKKTRARKWGERINLAGDVAALNSG
                     LATEAFSAYGNKTDNTREKRTHRRTKRFLSYPRFVEVLVVADNRMVSYHGENLQHYIL
                     TLMSIVASIYKDPSIGNLINIVIVNLIVIHNEQDGPSISFNAQTTLKNFCQWQHSKNS
                     PGGIHHDTAVLLTRQDICRAHDKCDTLGLAELGTICDPYRSCSISEDSGLSTAFTIAH
                     ELGHVFNMPHDDNNKCKEEGVKSPQHVMAPTLNFYTNPWMWSKCSRKYITEFLDTGYG
                     ECLLNEPESRPYPLPVQLPGILYNVNKQCELIFGPGSQVCPYMMQCRRLWCNNVNGVH
                     KGCRTQHTPWADGTECEPGKHCKYGFCVPKEMDVPVTDGSWGSWSPFGTCSRTCGGGI
                     KTAIRECNRPEPKNGGKYCVGRRMKFKSCNTEPCLKQKRDFRDEQCAHFDGKHFNING
                     LLPNVRWVPKYSGILMKDRCKLFCRVAGNTAYYQLRDRVIDGTPCGQDTNDICVQGLC
                     RQAGCDHVLNSKARRDKCGVCGGDNSSCKTVAGTFNTVHYGYNTVVRIPAGATNIDVR
                     QHSFSGETDDDNYLALSSSKGEFLLNGNFVVTMAKREIRIGNAVVEYSGSETAVERIN
                     STDRIEQELLLQVLSVGKLYNPDVRYSFNIPIEDKPQQFYWNSHGPWQACSKPCQGER
                     KRKLVCTRESDQLTVSDQRCDRLPQPGHITEPCGTDCDLRWHVASRSECSAQCGLGYR
                     TLDIYCAKYSRLDGKTEKVDDGFCSSHPKPSNREKCSGECNTGGWRYSAWTECSKSCD
                     GGTQRRRAICVNTRNDVLDDSKCTHQEKVTIQRCSEFPCPQWKSGDWSECLVTCGKGH
                     KHRQVWCQFGEDRLNDRMCDPETKPTSMQTCQQPECASWQAGPWGQCSVTCGQGYQLR
                     AVKCIIGTYMSVVDDNDCNAATRPTDTQDCELPSCHPPPAAPETRRSTYSAPRTQWRF
                     GSWTPCSATCGKGTRMRYVSCRDENGSVADESACATLPRPVAKEECSVTPCGQWKALD
                     WSSCSVTCGQGRATRQVMCVNYSDHVIDRSECDQDYIPETDQDCSMSPCPQRTPDSGL
                     AQHPFQNEDYRPRSASPSRTHVLGGNQWRTGPWGACSSTCAGGSQRRVVVCQDENGYT
                     ANDCVERIKPDEQRACESGPCPQWAYGNWGECTKLCGGGIRTRLVVCQRSNGERFPDL
                     SCEILDKPPDREQCNTHACPHDAAWSTGPWSSCSVSCGRGHKQRNVYCMAKDGSHLES
                     DYCKHLAKPHGHRKCRGGRCPKWKAGAWSQCSVSCGRGVQQRHVGCQIGTHKIARETE
                     CNPYTRPESERDCQGPRCPLYTWRAEEWQECTKTCGEGSRYRKVVCVDDNKNEVHGAR
                     CDVSKRPVDRESCSLQPCEYVWITGEWSEVPSWEL"
BASE COUNT     1471 a   1112 c   1362 g   1194 t
ORIGIN


alignment_scores:
            Quality:  422.00              Length:     70
              Ratio:  6.029                 Gaps:      0
 Percent Similarity: 100.000   Percent Identity: 100.000

alignment_block:
 US-09-972-467-2_COPY_509_578 x AB037733   ..

 Align seg 1/1  to: AB037733  from: 1  to: 5139

       1 GlnLeuProGlyIleLeuTyrAsnValAsnLysGlnCysGluLeuIlePh 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1052 CAACTGCCAGGCATCCTTTACAACGTGAATAAACAATGTGAATTGATTTT 1101

      17 eGlyProGlySerGlnValCysProTyrMetMetGlnCysArgArgLeuT 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1102 TGGACCAGGTTCTCAGGTGTGCCCATATATGATGCAGTGCAGACGGCTCT 1151

      34 rpCysAsnAsnValAsnGlyValHisLysGlyCysArgThrGlnHisThr 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1152 GGTGCAATAACGTCAATGGAGTACACAAAGGCTGCCGGACTCAGCACACA 1201

      51 ProTrpAlaAspGlyThrGluCysGluProGlyLysHisCysLysTyrGl 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1202 CCCTGGGCCGATGGGACGGAGTGCGAGCCTGGAAAGCACTGCAAGTATGG 1251

      67 yPheCysVal 70
         |||||||||
    1252 ATTTTGTGTT 1261

seq_name: gb_pat:AX319857

seq_documentation_block:
LOCUS       AX319857               5808 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 21 from Patent WO0183782.
ACCESSION   AX319857
VERSION     AX319857.1  GI:17901447
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```